

FIG. 1C

SpeI
 C C C G G T A C T A G T C C G A G C C G C C G A A A C C G C A G C C G C C G A G C C G A A 300

P G T S P Q P Q P K P Q P Q P Q P Q P K

Acc65I KpnI Eco52I
 C C G C A G C C G A A C C G G A A C C G G A A G G T A C C G G A T C A T C A G A A A A G A T G A G T I G T A G G C C G 360

P Q P K P E P E G T G S S E K D E L

NdeI Ppu10I BfrBI NsiI XhoI EcoRI SclI
 G C C G C A G A A T T C C A T A T G C A T C T C G A G 387

FIG. 1D

Bbr I EcoP15I
 HindIII NcoI EcoP15I
 AAGCTTACCAATCGGAAGATTCACTGTGGTGGCGCGCGTGTGCTGCTGCGCGCGGTG
 60
 M G K F T V V A A A L L L G A V
 BamHI
 TaqII' PshAI BpmI
 CGGGCCGAGGATCCAGCCCTGGGTGGAGACTGTGTCCACAGATGCTTCGAGAACTCCAG
 120
 R A E G S S L G G D C C C P Q M L R E L Q
 EcoICRI SacI BspMI BstZ2I EcHKI BstZ2I
 GAGACTAATGCGGCGCTGCAAGACGTGAGAGAGCTCTTGGCAGCAGCAGGTCAAGGAGATC
 180
 E T N A A L Q D V R E L L R Q Q V K E I
 EcoP15I Eco57I BsdMI
 ACCTTCCTGAAGAAATACCGGTGATGGAATGTGACCGCTTGGCGGAATGCAGCCCGCACGCC
 240
 T F L K N T V M E C D A C G M Q P A R T

FIG. 2C

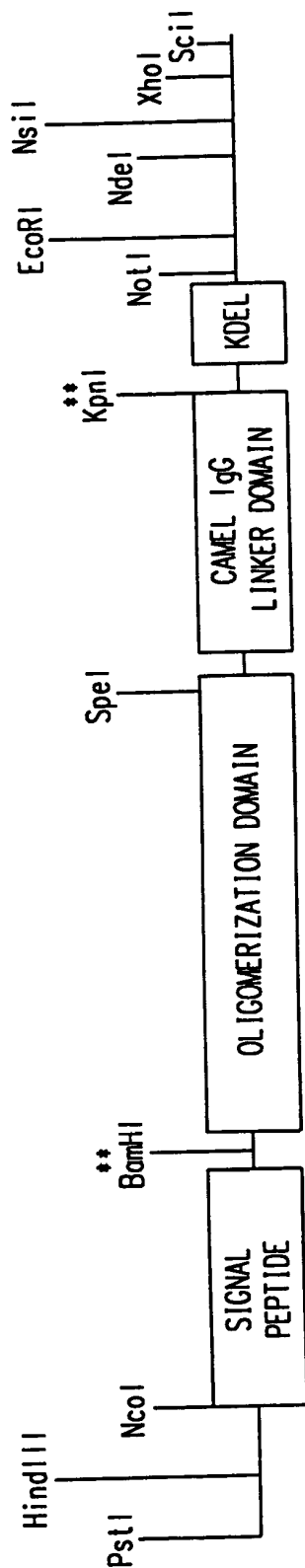


FIG. 3A

SIGNAL CLEAVAGE SITE

MCKFTVVAALLLLGAVRAE-GSS-

LGGDCC-KALVTQLTLFNQILVELRDDRQVKEMSLIRNTIMECQVCG-

PQPQKPQPQPQPQPKPEPE-GTGSSE-KDEL

FIG. 3B

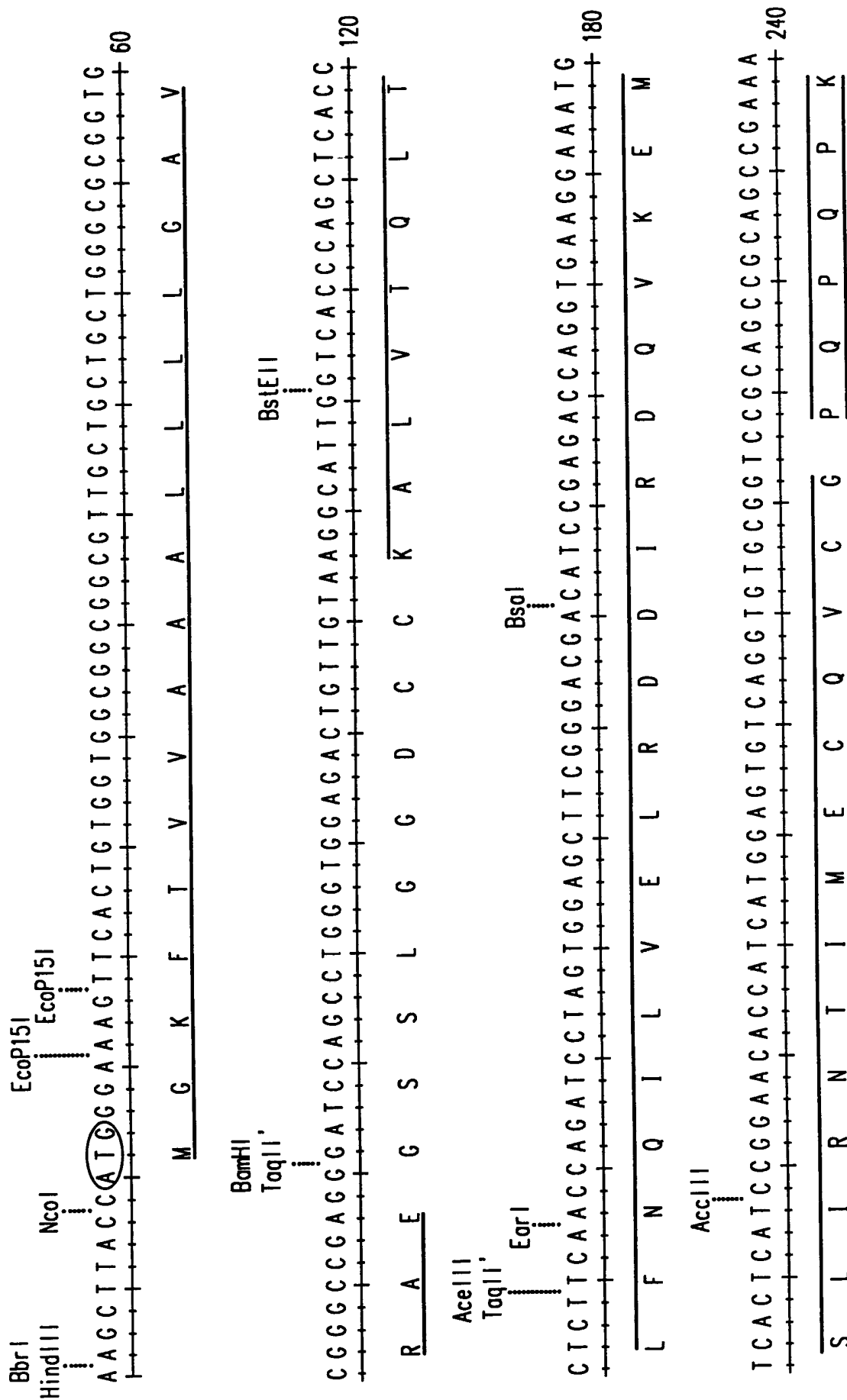


FIG. 3C

CCGCAGCCGCGCAGCCGCGCAGCCGCGAACC GGACCCGGAACTACC
 P Q P Q P Q P Q P Q P K P E P E G T

G S S E K D E L .
 GGATCATCAGAAAAGATGAGTTG TAGCGGCCCGCAGAAATTCCAATATGCATCTCGAG 357
 NdeI Ppu10I
 BfrBI
 NsiI
 XhoI
 Eco52I
 EcoRI
 SciI

SSSEKKDELL.

The diagram illustrates the CAMEL IgG construct, which is a fusion protein. It starts with a SIGNAL PEPTIDE domain, followed by an OLIGOMERIZATION DOMAIN, a CAMEL IgG LINKER DOMAIN, and a KDEL domain at the C-terminus. Various restriction enzyme sites are mapped along the construct: HindIII, PstI, NcoI, BamHI, SpeI, KpnI, EcoRI, NsiI, NdeI, XhoI, and SclI. The KDEL domain is shown as a separate box at the end of the construct.

SIGNAL CLEAVAGE SITE

M G K F T V V A A L L L G A V R A E - G S S -

LG G D C C - G E Q T K A L V T Q L T L F N Q I L V E L R D D I R D Q Q V K E M S L I R N T I M E C Q V C G -

POPOKPOPOPOPOPPQPKPPEPE - CTGSSE - KDEL

FIG. 4B

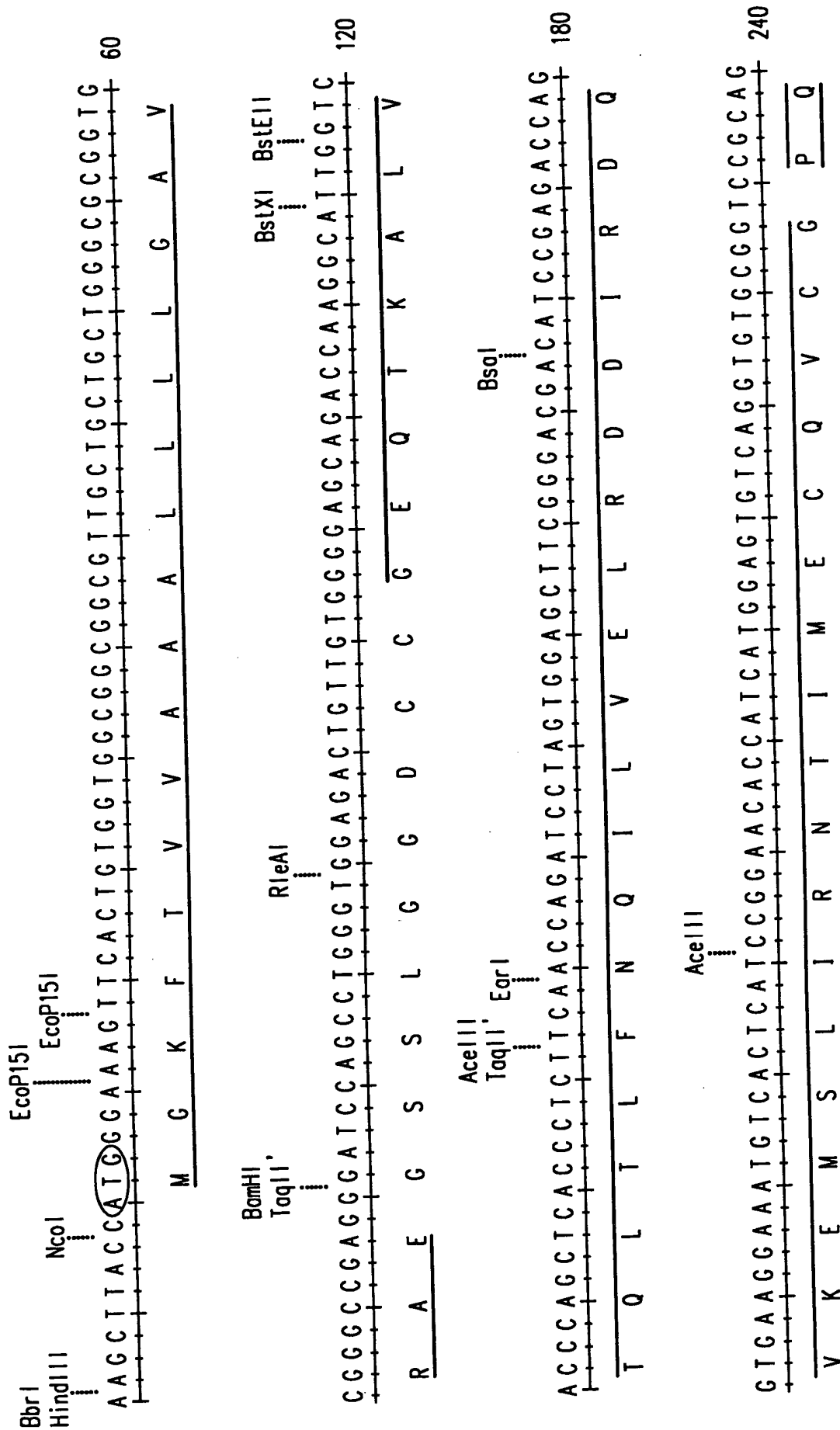


FIG. 4C

C C G C A G C C G A A C C G C A G C C G C C G C A G C C G A A C C G C A A C C G G A A

300

P Q P K P Q P Q P Q P Q P Q P Q P E

C C G G A A G G T A C C G G A T C A T C A G A A A A G A T G A G T T G T A G C C G G C C G C A G A A T T C C A T A T G 360
 NdeI Ppu10I BfrBI
 EcoRI
 Eco52I
 KpnI
 Acc65I

P E C T S S E K D E L .

NsiI
 XhoI
 SclI
 CATCTCGAG
 369

FIG. 4D

Diagram illustrating the structure of the CAMEL IgG construct. The construct consists of four domains: SIGNAL PEPTIDE, OLIGOMERIZATION DOMAIN, CAMEL IgG LINKER DOMAIN, and KDEL. Restriction sites are indicated by vertical lines above the construct: HindIII, PstI, NcoI, BamHI, SpeI, KpnI, EcoRI, NsiI, NotI, NdeI, XhoI, and SclI.

SIGNAL CLEAVAGE SITE

MGKFTVVAAALLLGAVRAE-GSS-

LGGDCC-GDVSRLICQITQMNLGELRDVMRQQVKETMFLRNTIAECQACG-

P O P K P O P O P K P O P E - G T G S S E - K D E L

FIG. 5B

FIG. 5C

000001 02030300

CCGAGCCGAACCGCAGCCGCGCAGCCGCGAACCAGCCGAAACCCGAAACCCGAA 300
 P Q P K P Q P Q P Q P Q P K P Q P K P E

CCGGAAGGTACCGGATCATCAGAAAGATGAGTTGTAGCCGGCCGCGCAGAAATCCATATG 360
 P E G T G S S E K D E L .
 NdeI Ppu10I BfrBI
 EcoRI
 Eco52I

NsiI
 XhoI
 SclI
 CATCTCGAG 369

FIG. 5D

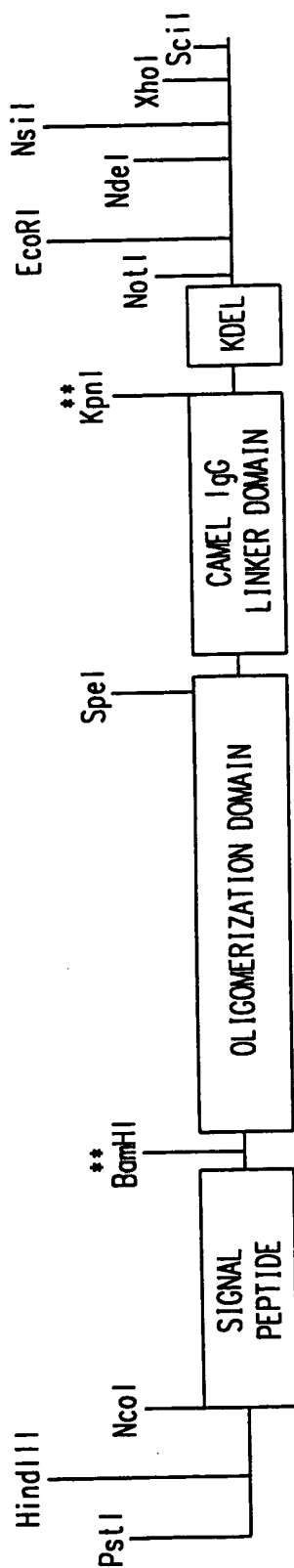


FIG. 6A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A V C S A A K K - G S S -

L G G D C C - S D L G P Q M L R E L Q E T N A A L Q D V R D W L R Q Q V R E I T F L K N T V M E C D A C G -

P Q P Q K P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

FIG. 6B

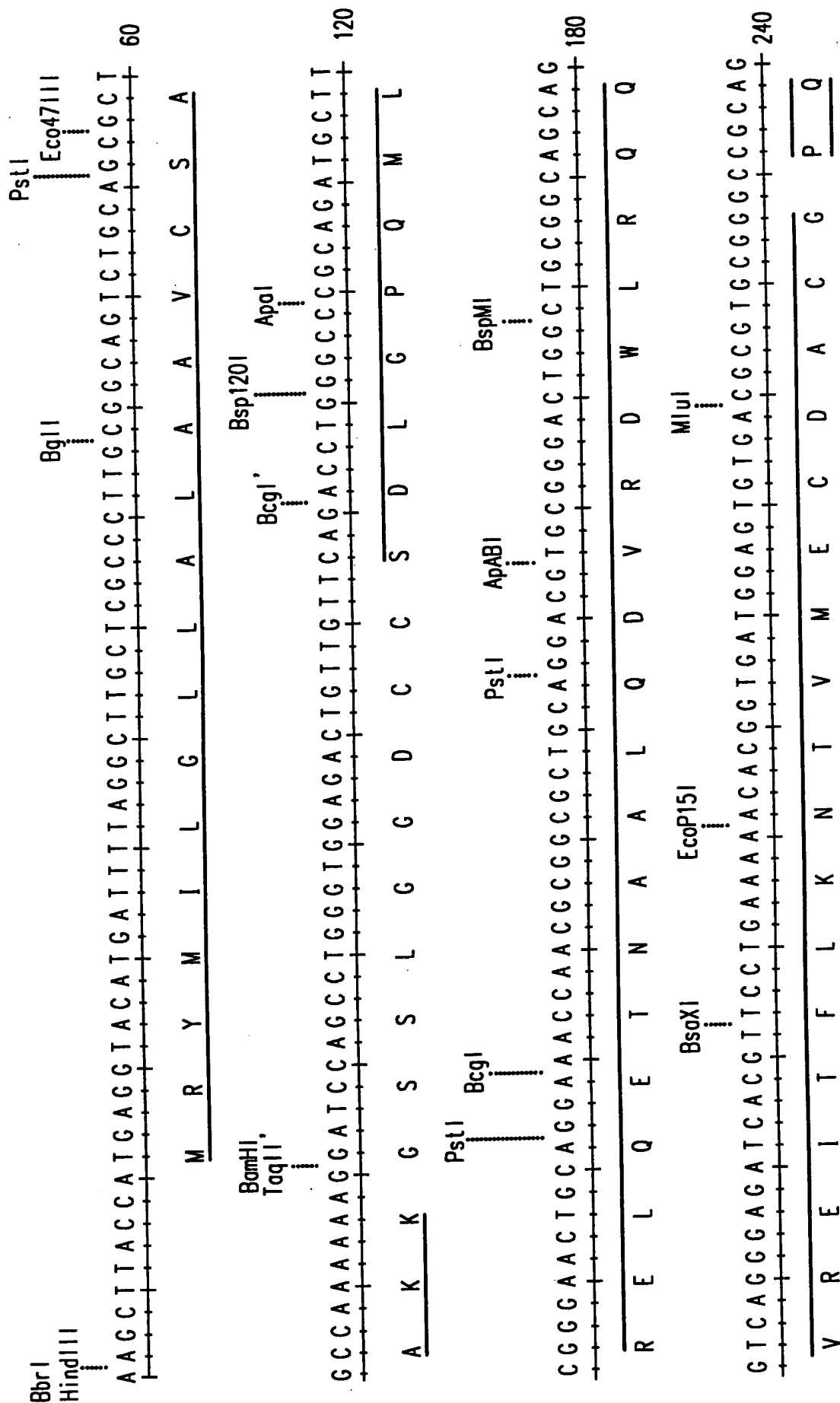


FIG. 6C

CCGCGAGCCGA AACCGCAGCCGCAGCCGCAGCCGAACCGCGAA
300

P	P
Q	Q
K	K
P	P
Q	Q
P	P
Q	Q
P	P
Q	Q
P	P
E	E

CCGGAAGGTACCGGATCATCAGAAAAGATGAGTTGTAGCGCGCCGACAGAAATTCATATG
 360
 NdeI Ppu10I BfrBI
 Eco52I EcoRI
 KpnI Acc65I

P E T E R S E N D E L

A schematic diagram of a 369 bp DNA fragment. The DNA sequence is represented by a horizontal line with vertical tick marks. The sequence 'CATCTCGAG' is written vertically below the line. Three restriction sites are indicated by vertical lines and labels: 'NsiI' at the left end, 'XhoI' in the middle, and 'SclI' at the right end. The 'SclI' site is located just before the 'CATCTCGAG' sequence. An arrow at the right end of the line points to the number '369'.

FIG. 6D

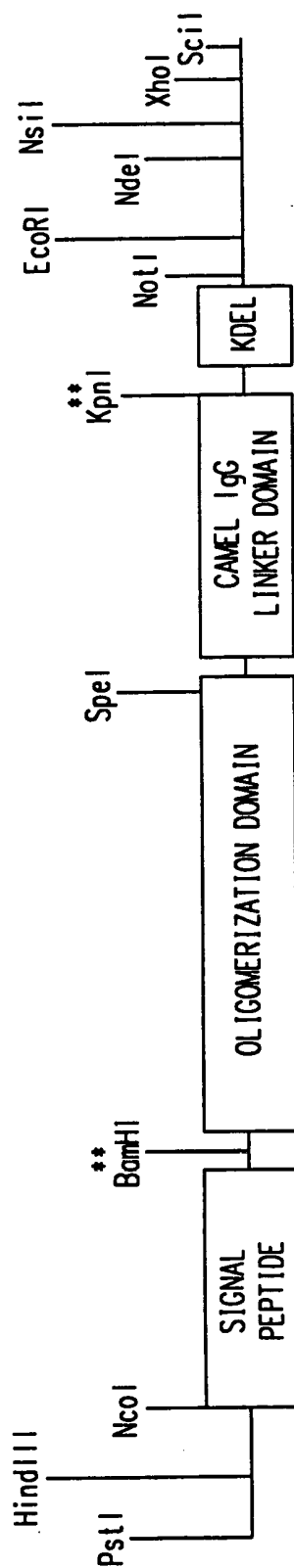


FIG. 7A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A A V C S A A K K - G S S -

L G G D C C - Q K L Q N L F I N F C I I L I C L L I C I I V M L L -

P Q P Q K P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

• RESIDUES CRITICAL FOR PENTAMER FORMATION

FIG. 7B

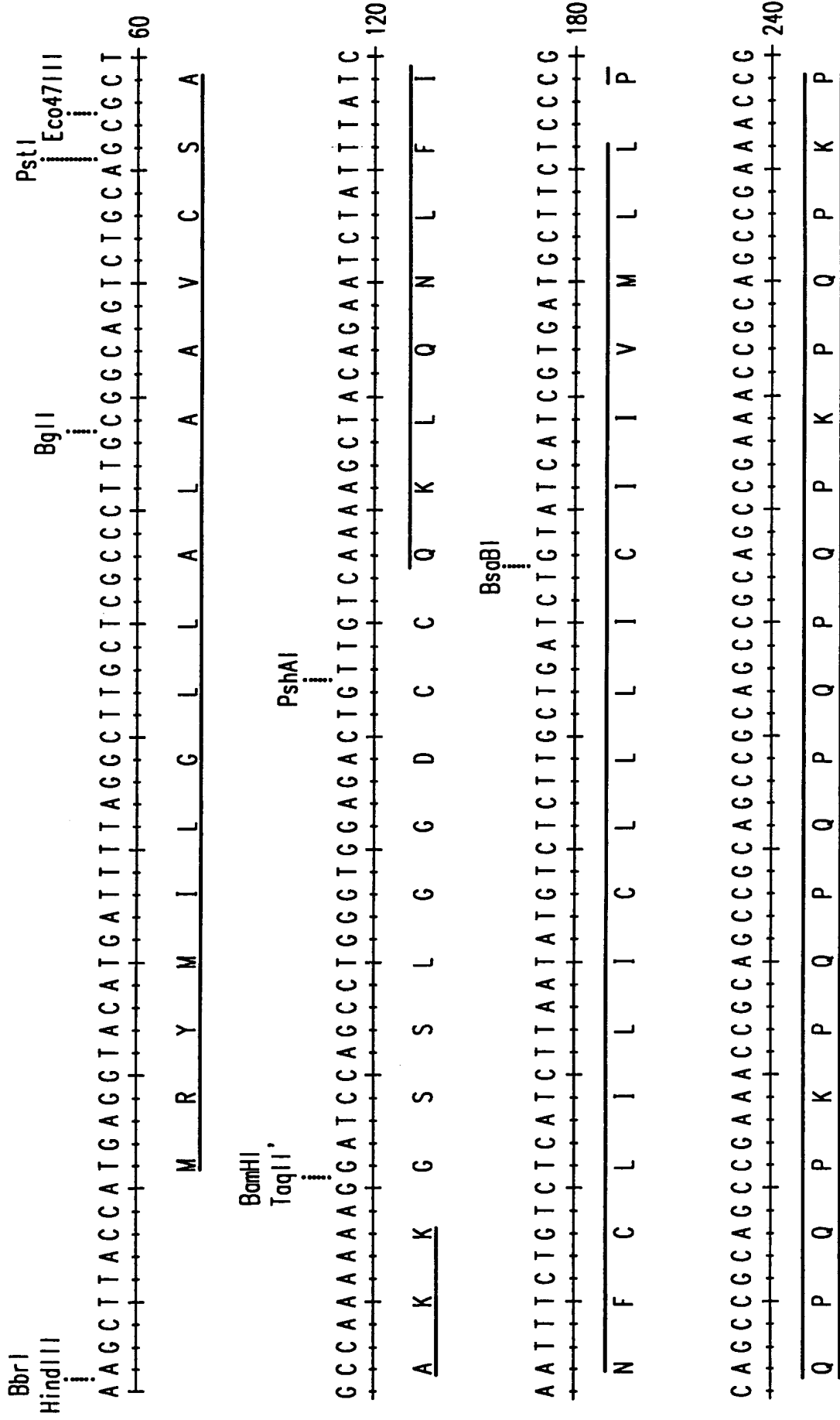
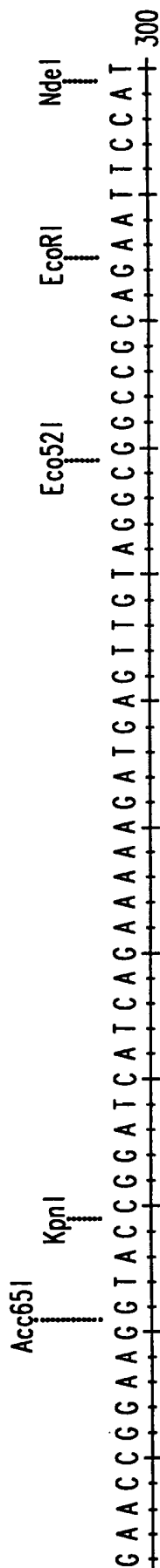


FIG. 7C



E P E G T G S S E K D E L

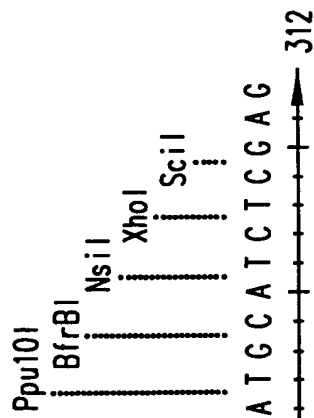


FIG. 7D

SIGNAL CLEAVAGE SITE

MRYMILGLLALA AVCSAAKK-GSS-

LGDCCC-GEQTKALVTQLTLFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-

[illegible]

FIG. 8B

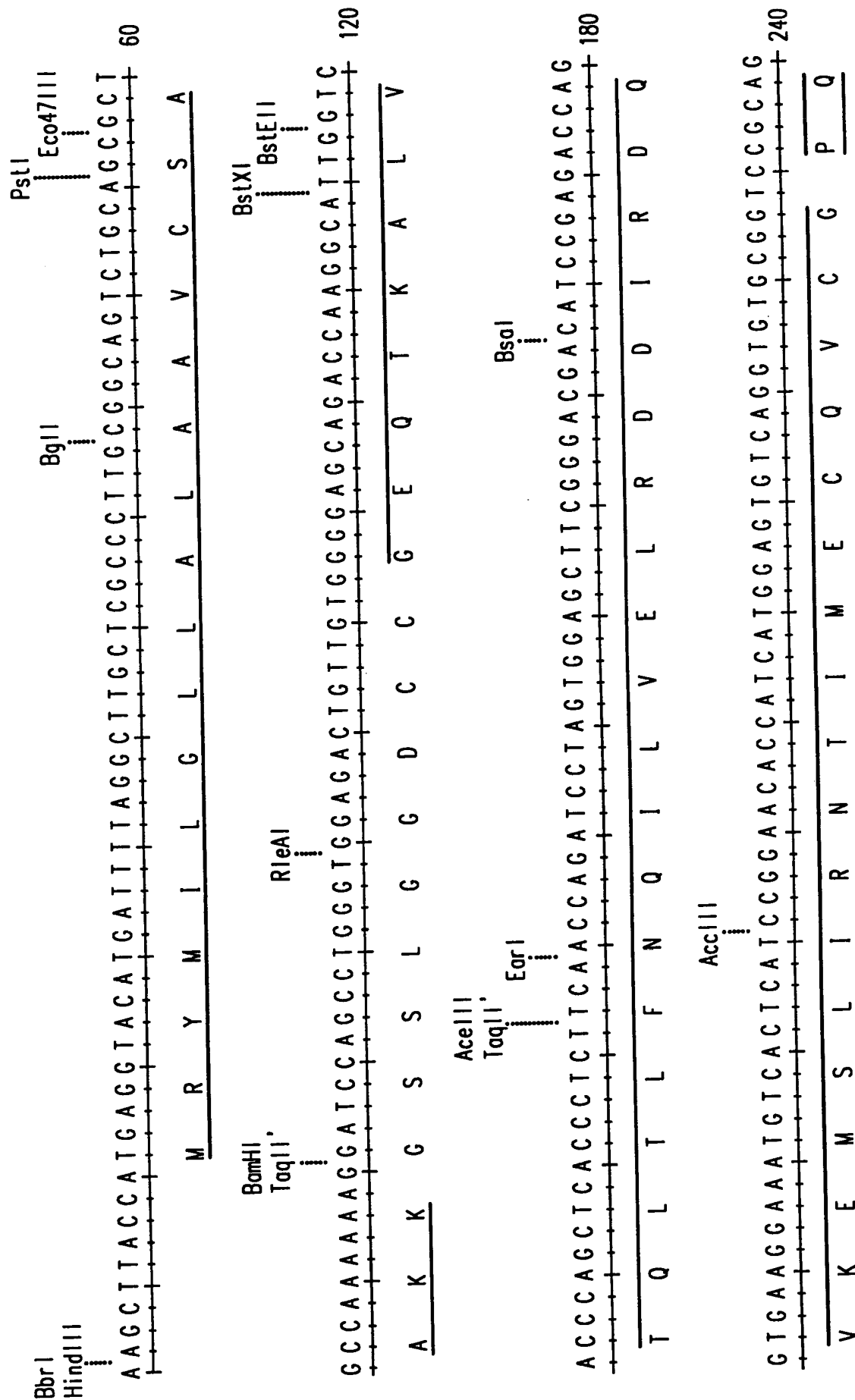


FIG. 8C

C C G C A G C C G A A C C G C A G C C G C A G C C G A A C C G G A A

P Q P K P Q P Q P Q P Q P Q P Q P Q

NdeI
 Ppu10I
 BfrBI
 EcoRI
 Eco52I
 KpnI
 Acc65I
 C C C G A A G G T A C C G G A T C A T C A G A A A A G A T G A G T T G T A G C C G C C G C A A T T C C A T A T G 360

P E C T C S S E K D E L .

Diagram illustrating the restriction enzyme sites for NsiI, XhoI, and SclI on the DNA sequence: CATCTCGAG. The NsiI site is at the beginning (C), XhoI is at the end (G), and SclI is in the middle (TCT).

• • • • •

Xhol

Si

CATCTCGAG → 369

FIG. 9C

C C G C A G C C G A A C C G C A G C C G C A G C C G C A G C C G A A C C G C A G C C G A A C C G C A

P Q P K P Q P Q P Q P Q P Q P Q P Q

CCGGAAGGTACCGGATCATCAGAAAGAGATGAGTTGTAGCGCGCCGACAGATTCCATATG360

Acc65I KpnI Eco52I EcoRI NdeI Ppu10I BfrBI

P E C T G S S E K D E L .

Diagram illustrating the DNA sequence CATCTCGAG with restriction sites NsiI, XhoI, and SclI marked by vertical lines. The sequence is shown as a horizontal line with tick marks. The restriction sites are indicated by vertical lines above the sequence: NsiI at the first position, XhoI at the second position, and SclI at the third position. The sequence ends with the number 369.

FIG. 9D

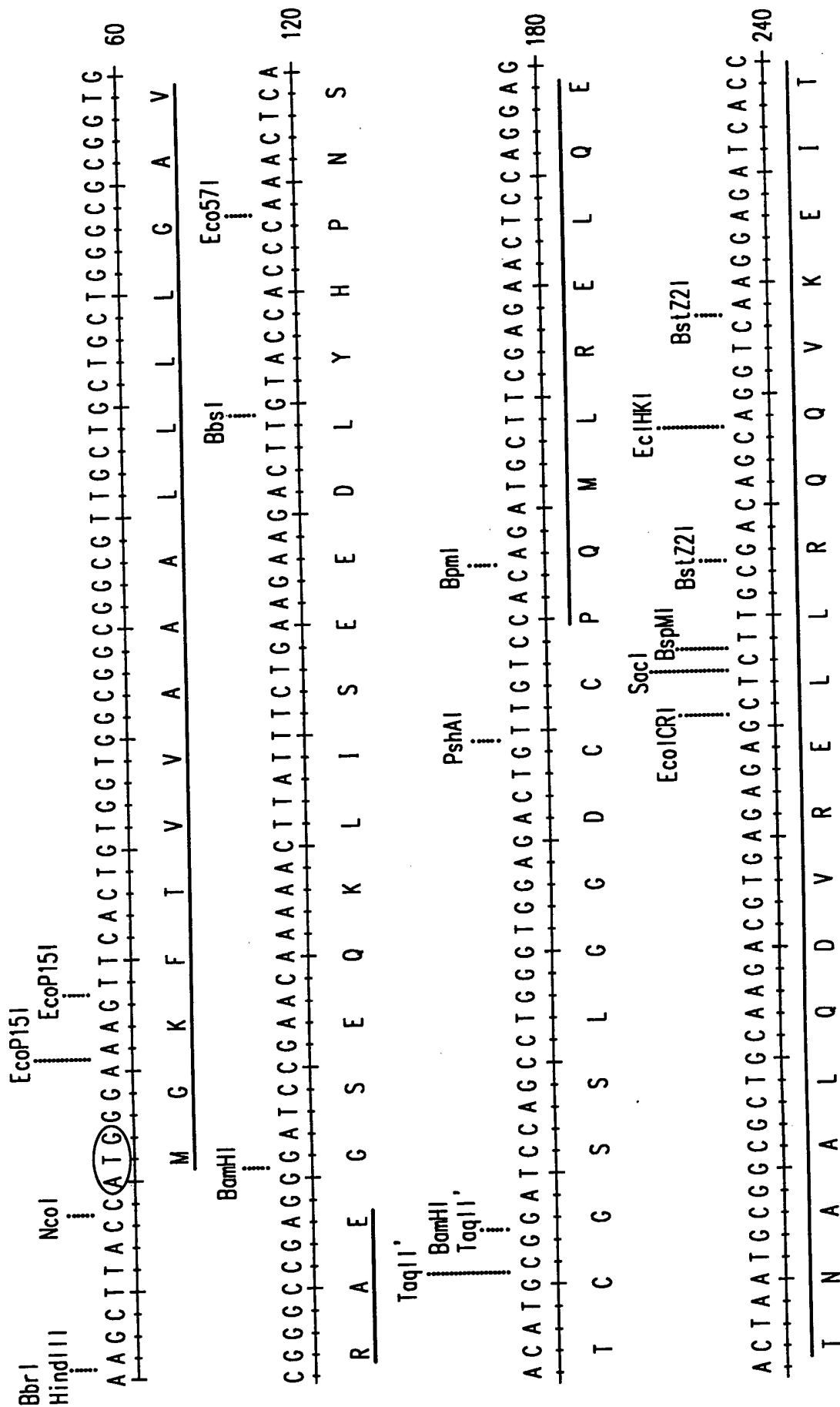
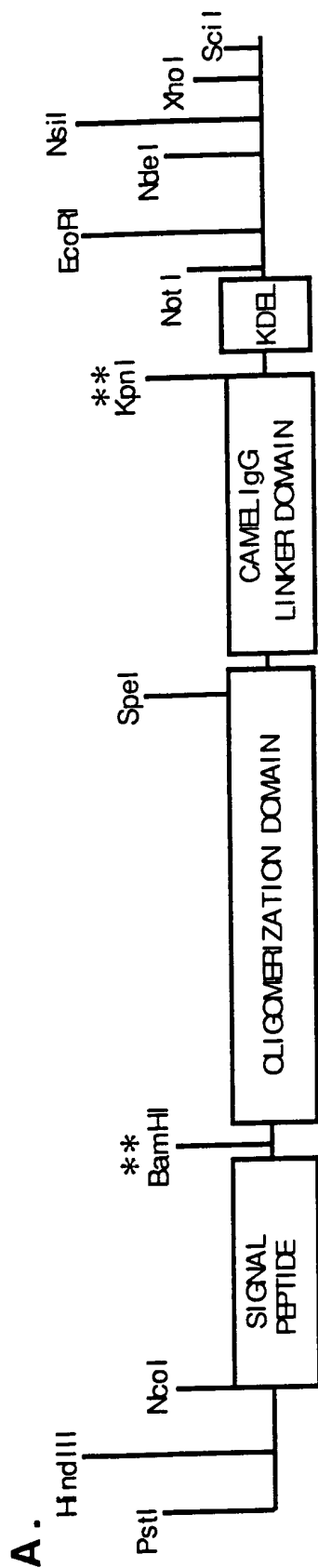


FIG.10C

Figure 1: Schematic Representation of KDEL Receptor-Inhibitor Protein and Its Amino Acid Sequences (Rat COMP oligomerization domain)



B.

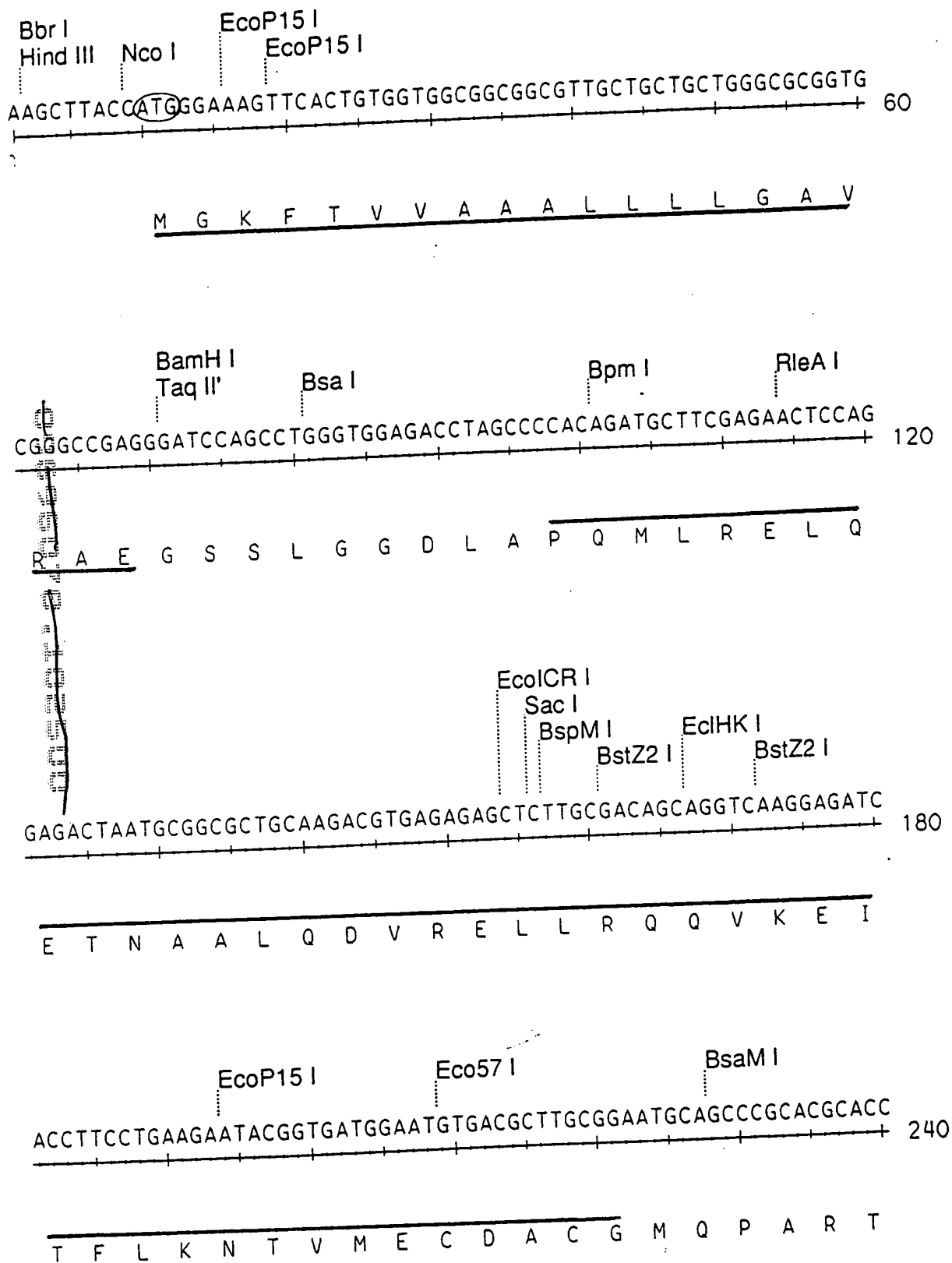
Signal cleavage site

MGKFTVVAALLLLGAVRAE-GSS -

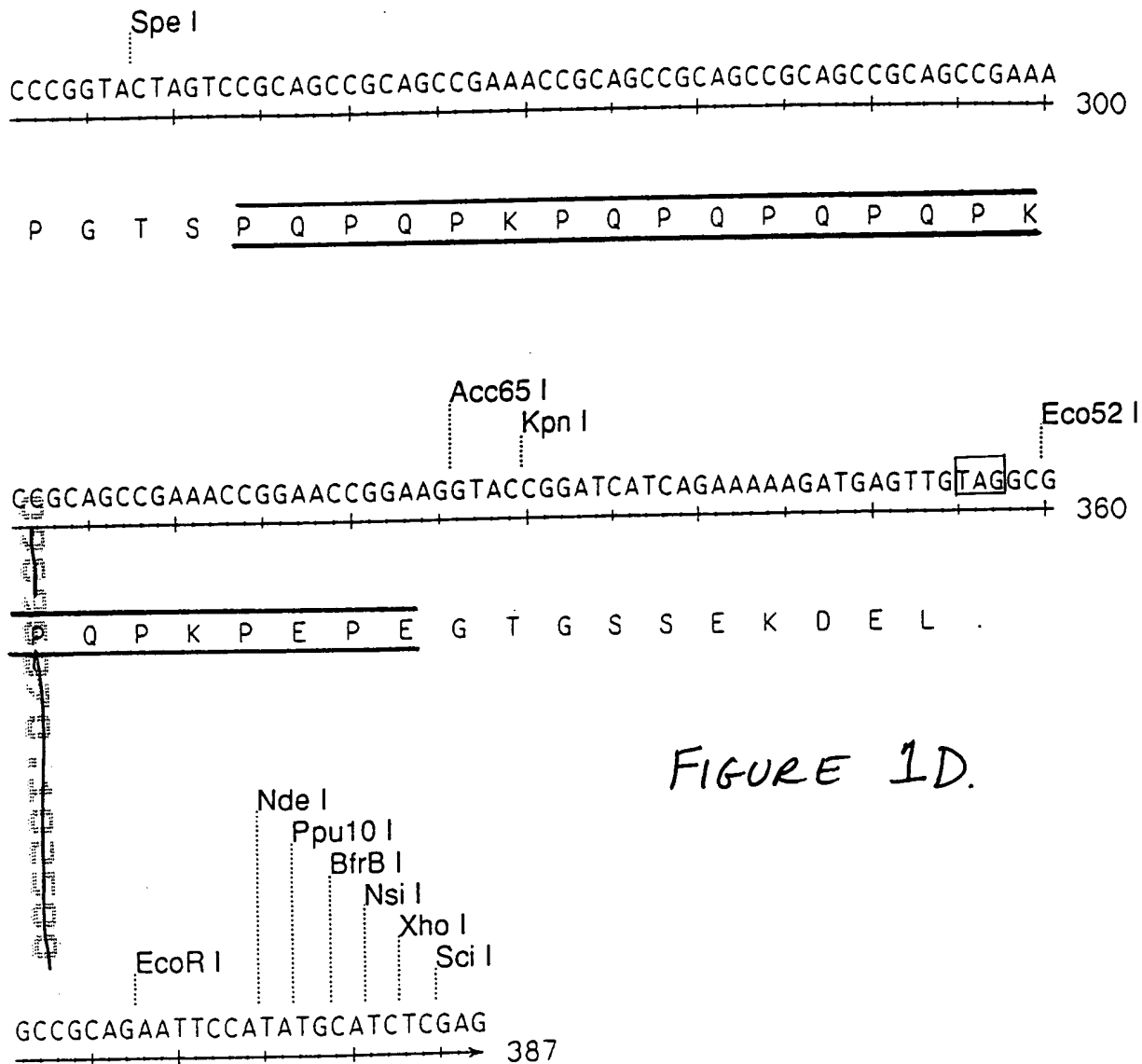
LGGDLA-PQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDACG-MQPARTPGTS-

PQPQPKPQPQPQPQPKPEPE-GTGSSE-KDEL

FIGURE 1C.

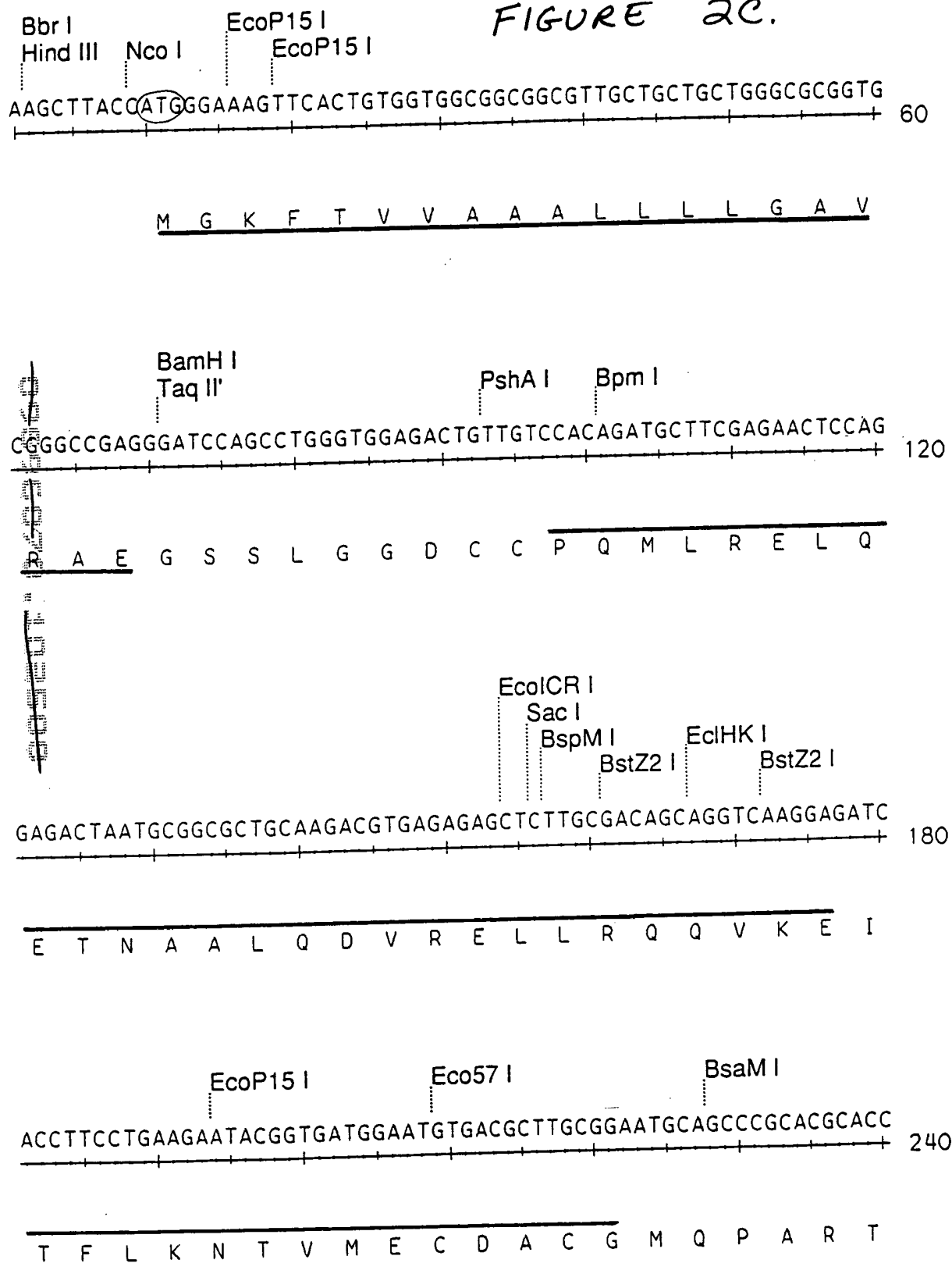


314f8 (sheet 3 of 3)



31:88 (sheet 5 of 30)

FIGURE 2C.



314.8 (sheet 6 of 30)

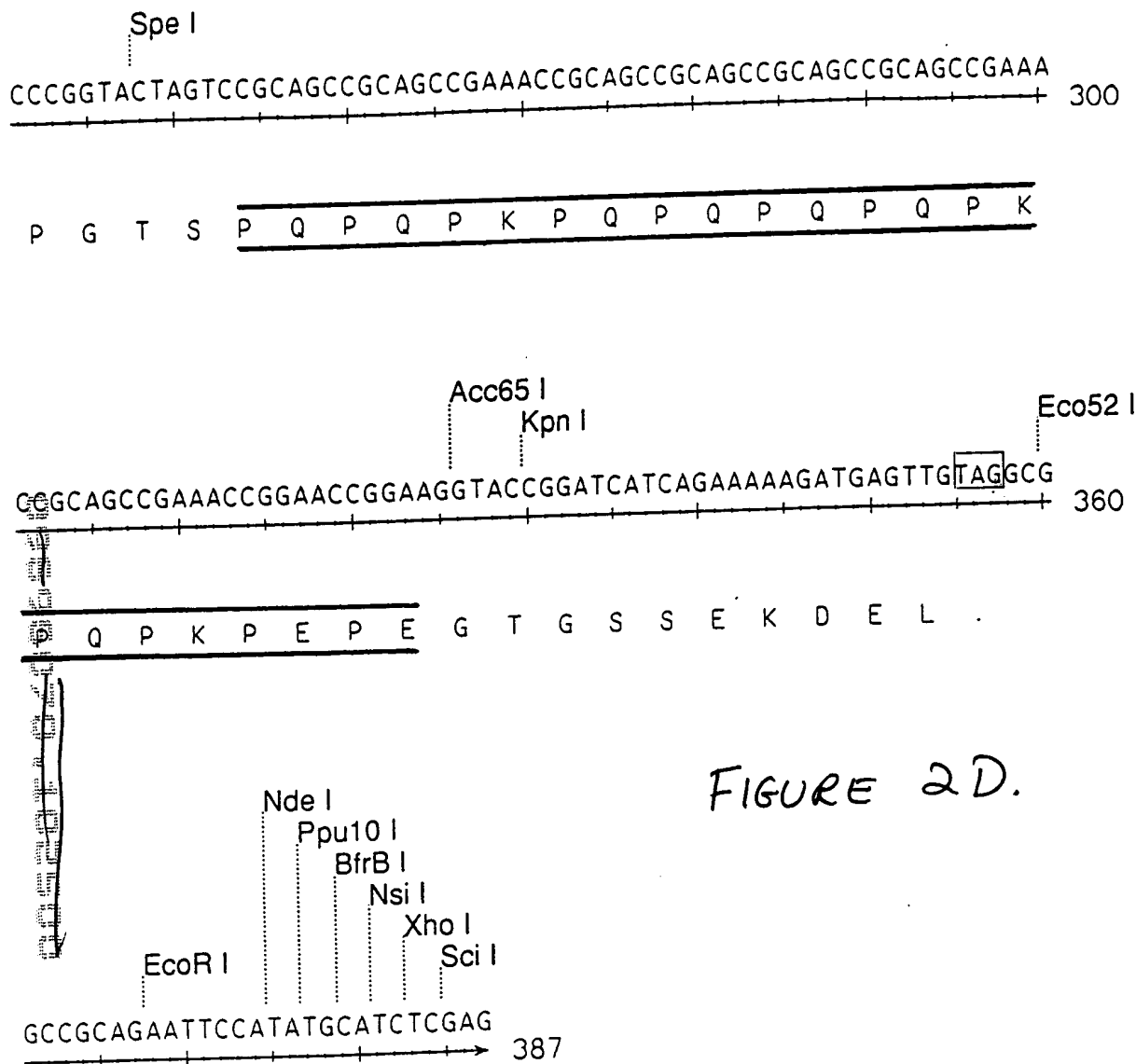
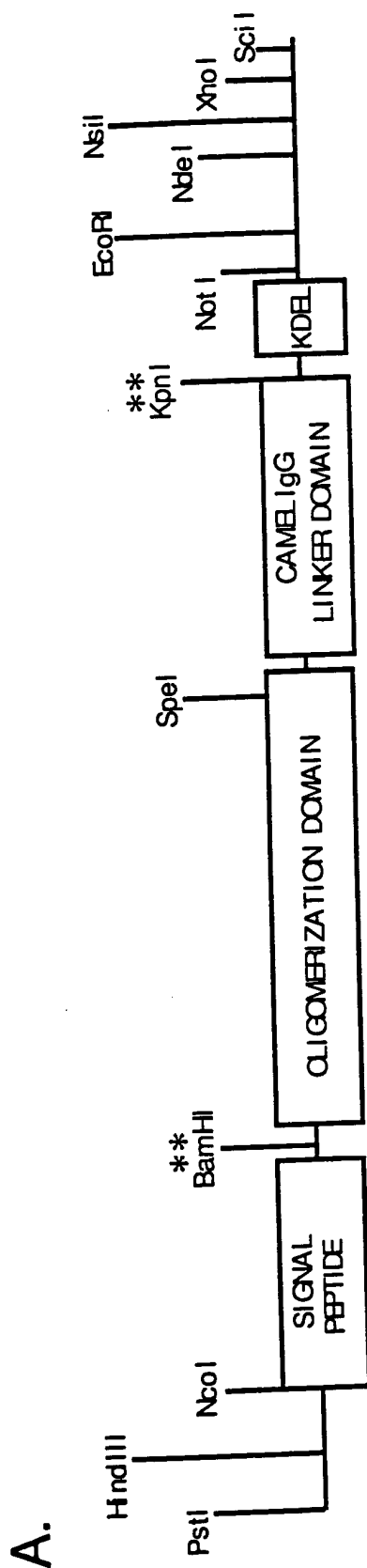


FIGURE 2D.

Figure 3: MOUSE TSP3 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

MGKFTVVAALLLLGAVRAE-GSS -

LGGDCC-KALVTQLTFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-

PQPQKPQPQPQPQPKPQKPEPE-GTGSSE-KDEL

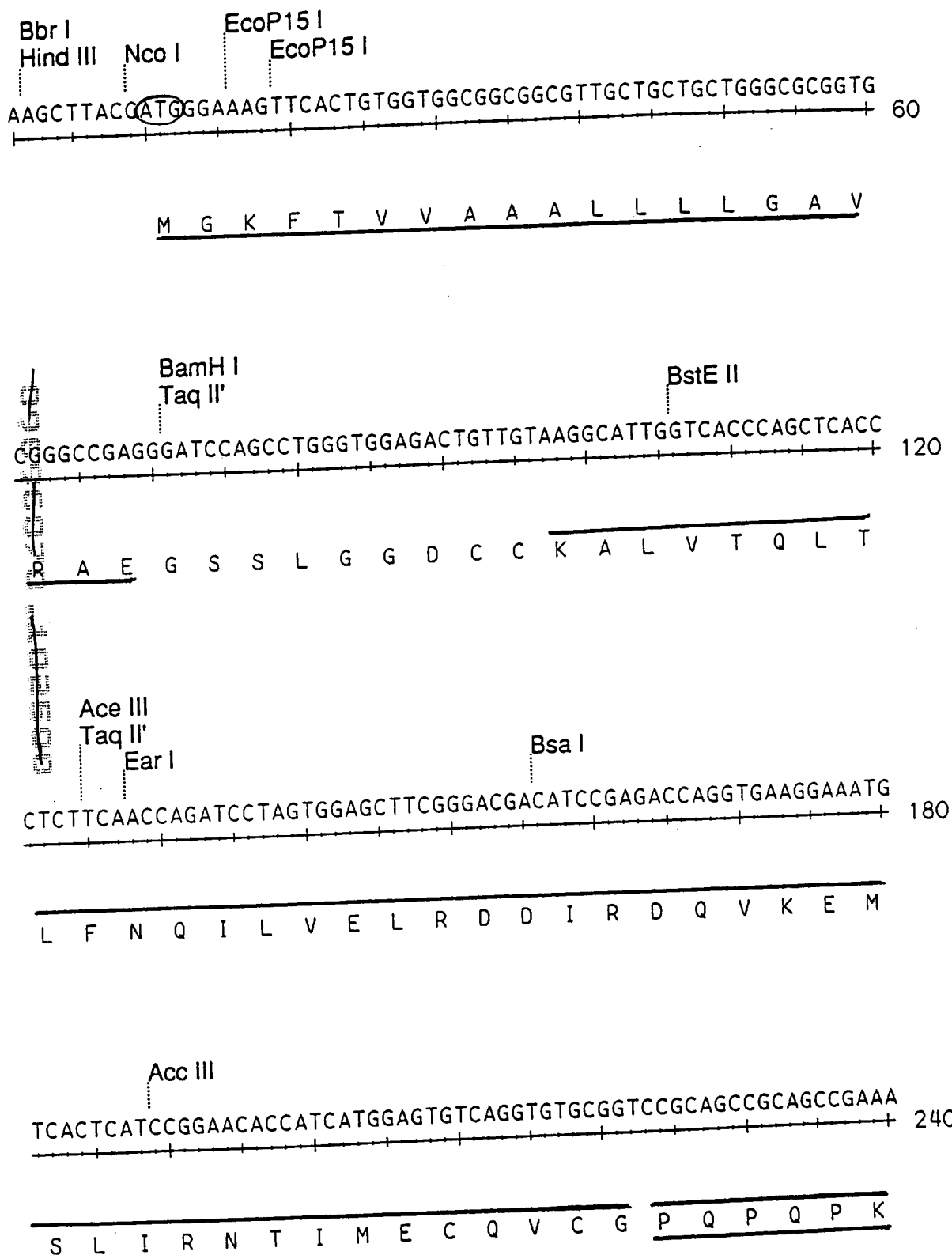


FIGURE 3C.

31488 (sheet 9 of 30)

CCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAACCGGAAGGTACC 300
Acc65 I
Kpn I

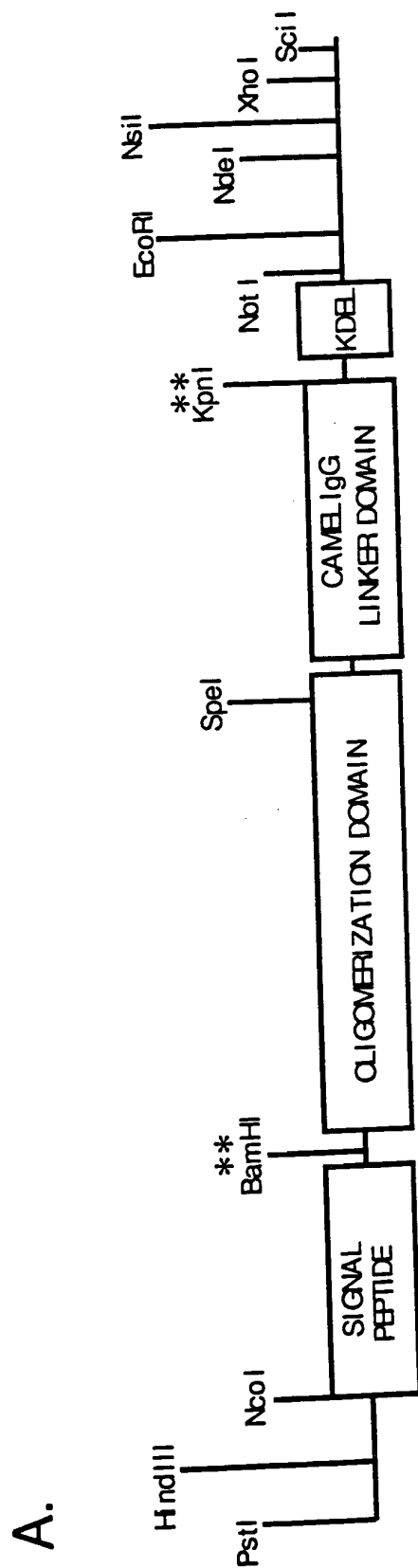
P Q P Q P Q P Q P K P Q P K P E P E G T

GGATCATCAGAAAAAGATGAGTTG TAG GCGGCCGCAGAATTCCATATGCATCTCGAG 357
Eco52 I EcoR I Nde I Ppu10 I BfrB I Nsi I Xho I Sci I

G S S E K D E L .

FIGURE 3D.

Figure 4: MOUSE TSP3 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

MGKFTVVAALLLLGAVRAE-GSS -

LGGDCC-GEQTKALVTQLTLFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-

PQPQPKPQPQPQPQPKPQPKPEPE-GTGSSE-KDEL

31488 (sheet 11 of 30)

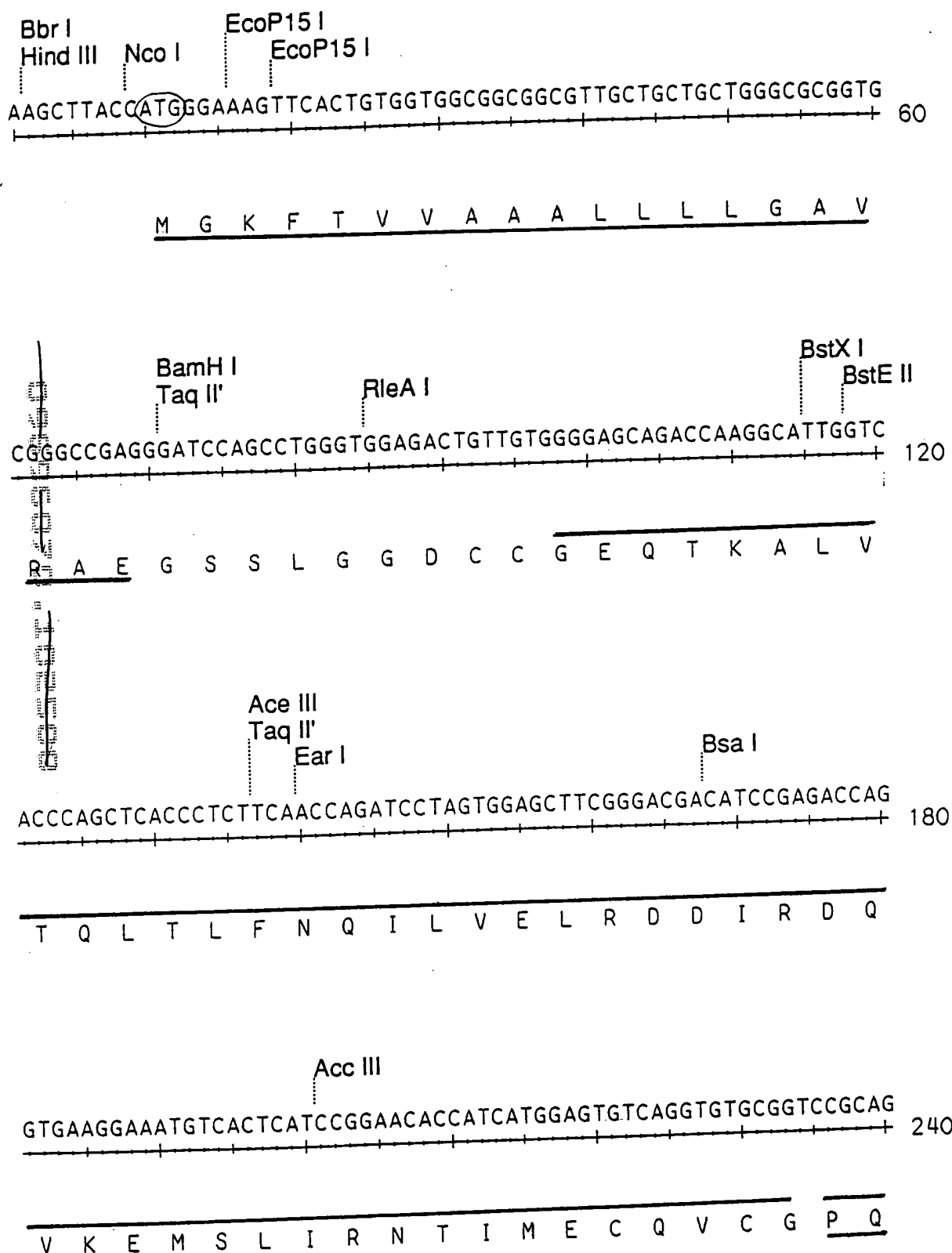


FIGURE 4C.

31,88 (sheet 12 of 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

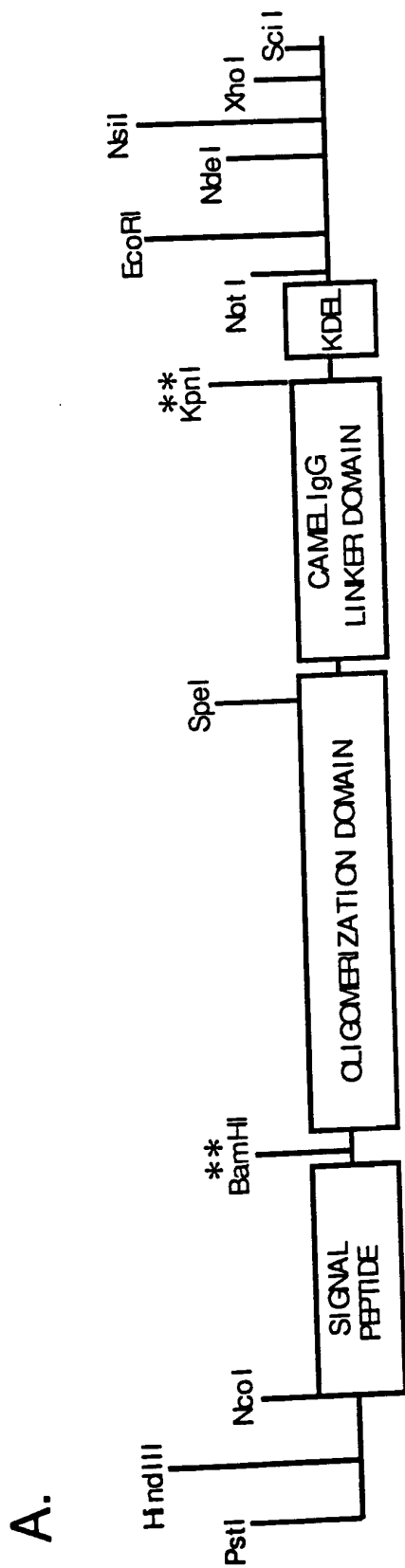
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
 CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG TAG GCGGCCGCAGAATTCCATATG 360

P E G T G S S E K D E L .

Nsi I Xho I Scl I
 CATCTCGAG 369

FIGURE 4D.

Figure 5: XENOPUS TSP4 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

MGKFTVVAALLLLGAVRAE-GSS -

LGGDCC-GDVSRQLIGQITQMNQMLGELRDVMRQQVKETMFLRNTIAECQACG-
PQPQKPQPQPQPQPKPQKPEPE-GTGSSE-KDEL

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Bbr I
Hind III Nco I EcoP15 I
EcoP15 I
AAGCTTACCATGGGAAAGTTCACTGTGGTGGCGGCGGCGTTGCTGCTGCTGGGCGCGGTG 60

M G K F T V V A A A L L L L G A V

BamH I
Taq II' Aat II Msp20 I
CGGGCCGAGGGATCCAGCCTGGGTGGAGACTGTTGTGGTGACGTCAGCAGACAGTTGATT 120

R A E G S S L G G D C C G D V S R Q L I

Bal I Msp20 I EcoP15 I AlwN I EcoICR I
Sac I BspH I
BspM I
GGCCAGATAACCCAAATGAATCAGATGCTGGGAGAGCTCCGAGATGTCATGAGACAGCAG 180

G Q I T Q M N Q M L G E L R D V M R Q Q

Bsa I EcoP15 I BsrD I Bce83 I
BsaM I Stu I BstX I
GTGAAAGAGACCATGTTCTTGAGAAACACCATTGCAGAATGCCAGGCCTGTGGCCCGCAG 240

V K E T M F L R N T I A E C Q A C G P Q

FIGURE 5C

31488 (sheet 15 of 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P K P Q P K P E

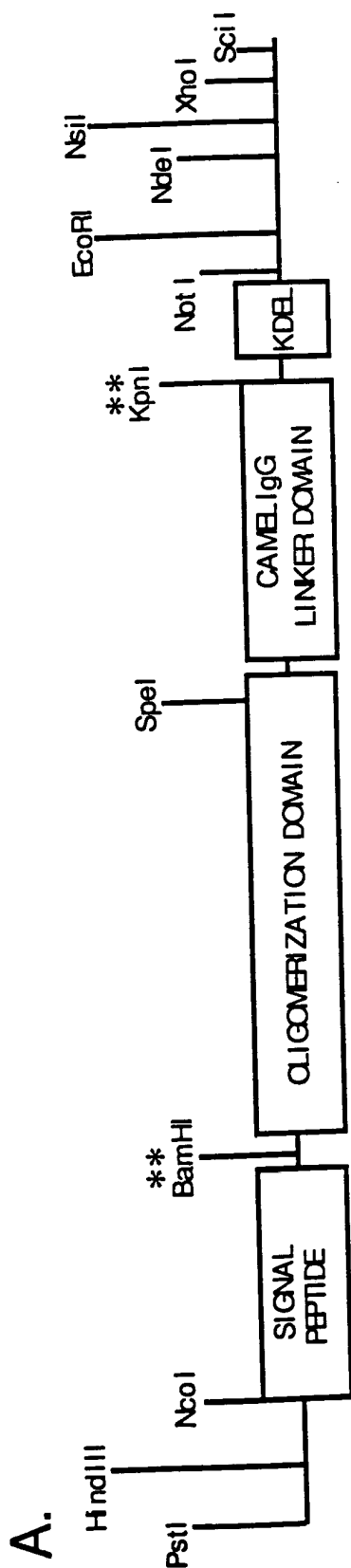
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG TAG GCGGCCGCAGAATTCCATATG 360
ATAC

P E G T G S S E K D E L .

Nsi I Xho I Scl I
CATCTCGAG 369

FIGURE 5D.

Figure 6: HUMAN COMP OLIGOMERIZATION DOMAIN
KDEL RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

↓

MRYMILGLLALAAVCSAAKK-GSS -

LGGDCC-SDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNTVMECDACG-

PQPQKPQPQPQPQPQPQPPEPE-GTGSSE-KDEL

31488 (sheet 17 of 30)

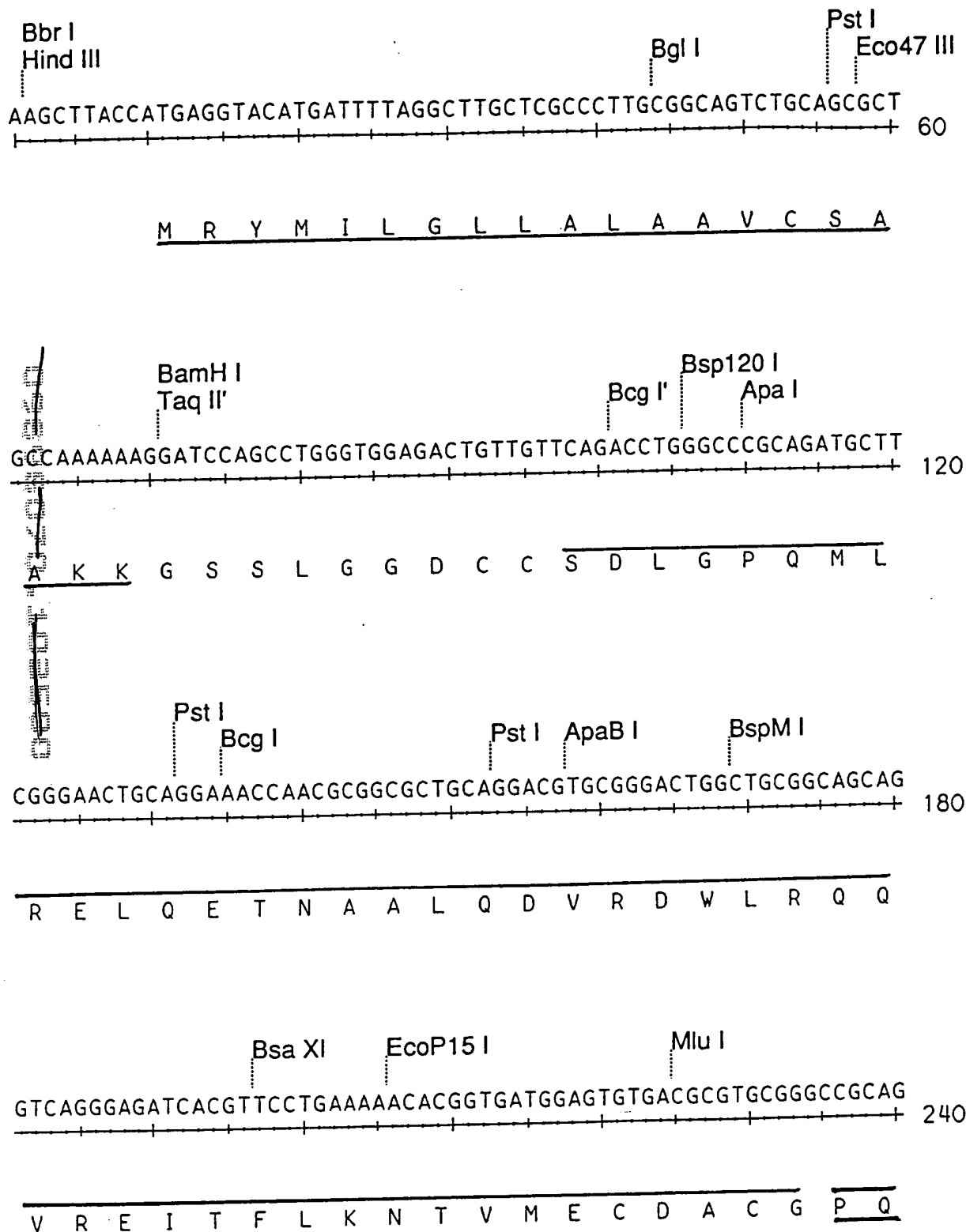


FIGURE 6C.

31488 (sheet 18 of 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

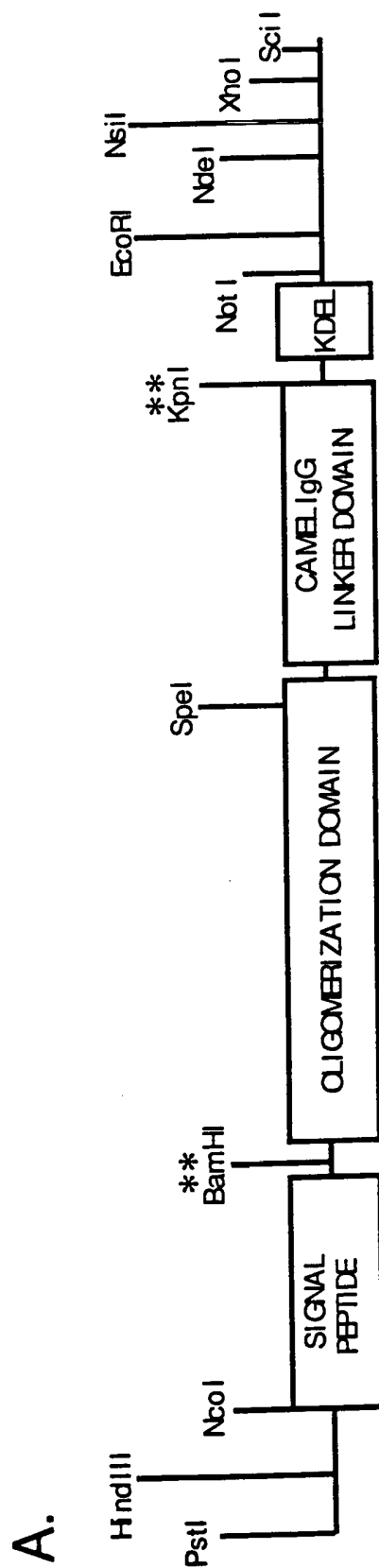
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360

P E G T G S S E K D E L .


Nsi I Xho I Sci I
CATCTCGAG 369

FIGURE 6D.

Figure 7: HUMAN PLB OLIGOMERIZATION DOMAIN KDEL RECEPTOR INHIBITOR PROTEIN



മ്

Signal cleavage site

MRYMILGLLAAVCSAKK-GSS-

LGGDCC-QKLQNLFINFCLILICLLLCIIVMLL-

PQQPKPQPQPQPKPQPKPEPE-GTGSSE-KDEL

- Residues critical for pentamer formation

3.488 (sheet 20 of 30)

Bbr I
Hind III
Bgl I
Pst I
Eco47 III

AAGCTTACCATGAGGTACATGATTTTAGGCTTGCTCGCCCTTGCGGCAGTCTGCAGCGCT 60

M R Y M I L G L L A L A A V C S A

BamH I
Taq II'
PshA I

GC CAAAAAAGGATCCAGCCTGGGTGGAGACTGTTGTCAAAGCTACAGAATCTATTTATC 120

A K K G S S L G G D C C Q K L Q N L F I

BsaB I

AATTTCTGTCTCATCTTAATATGTCTCTTGCTGATCTGTATCATCGTGATGCTTCTCCCG 180

N F C L I L I C L L I C I I V M L L P

CAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCG 240

Q P Q P K P Q P Q P Q P Q P K P Q P K P

FIGURE 7C.

51488 (sheet 21 of 30)

Acc65 I Kpn I Eco52 I EcoR I Nde I

GAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCAT 300

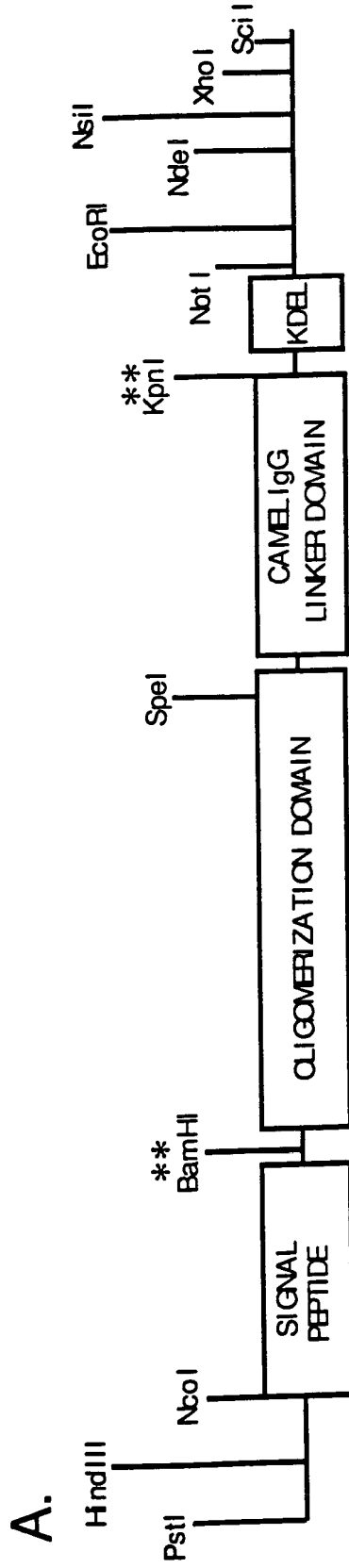
E P E G T G S S E K D E L .

Ppu10 I
BfrB I
Nsi I
Xho I
Sci I

ATGCATCTCGAG 312

FIGURE 7D.

Figure 8: HUMAN TSP3 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

↓

MRYMILGLLALAAVCSAAKK-GSS -

LGGDCC-GEQTKALVTQLTLFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-

PQPQPKPQPQPQPQPKPQPKPEPE-GTGSSE-KDEL

31488 (sheet 23 of 30)

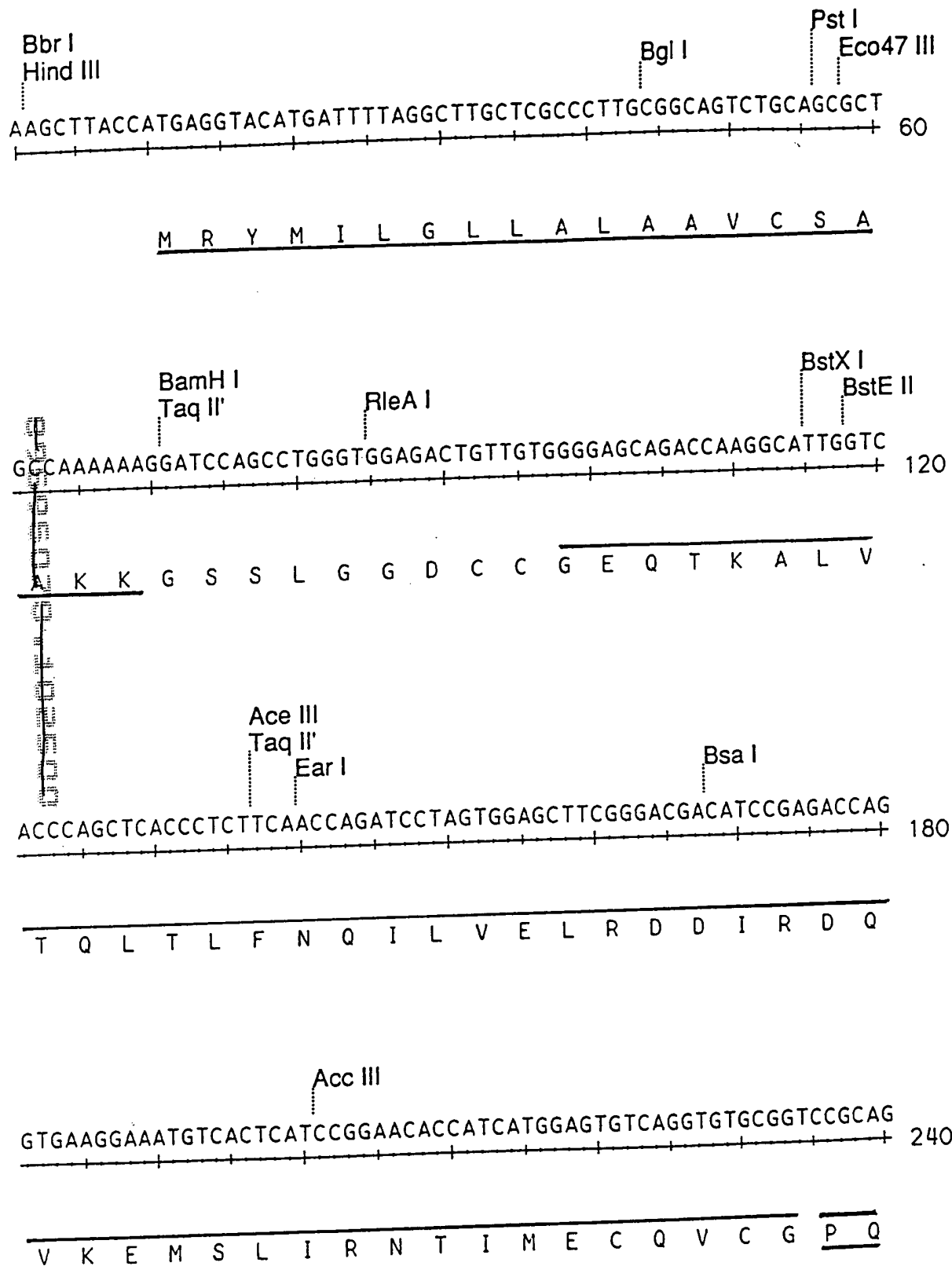


FIGURE 8C.

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CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

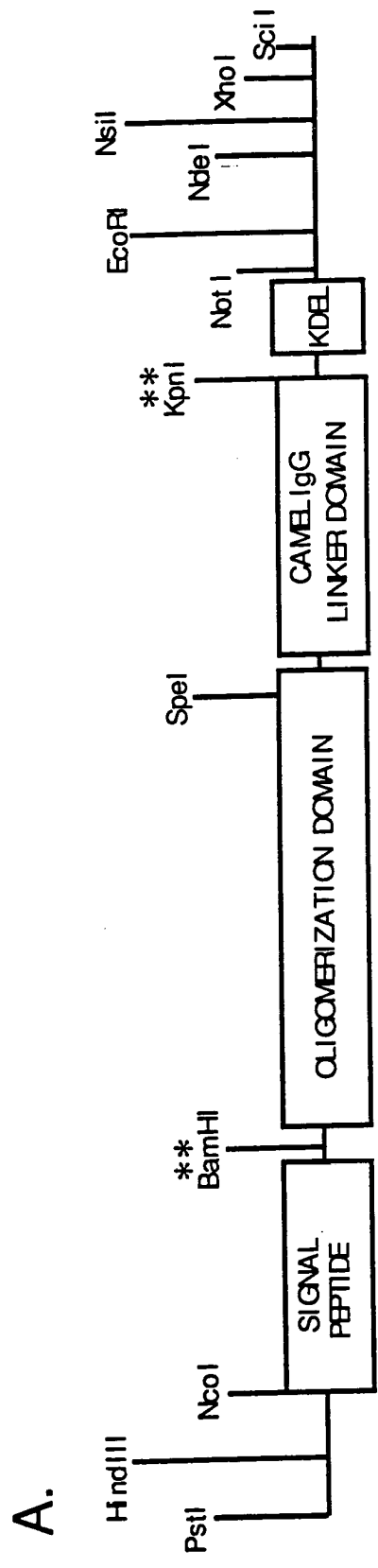
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360

P E G T G S S E K D E L .

Nsi I Xho I Sci I
CA ECTCGAG 369

FIGURE 8D.

Figure 9: HUMAN TSP4 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

↓

MRYMILGLLALAAVCSAAKK-GSS -

LGGDCC-GDFNRQFLGQMTQLNQLLGEVKDLLRQQVKETSFRLNTIAECQACG-

PQPQPKPQPQPQPQPKPQPKPEPE-GTGSSE-KDEL

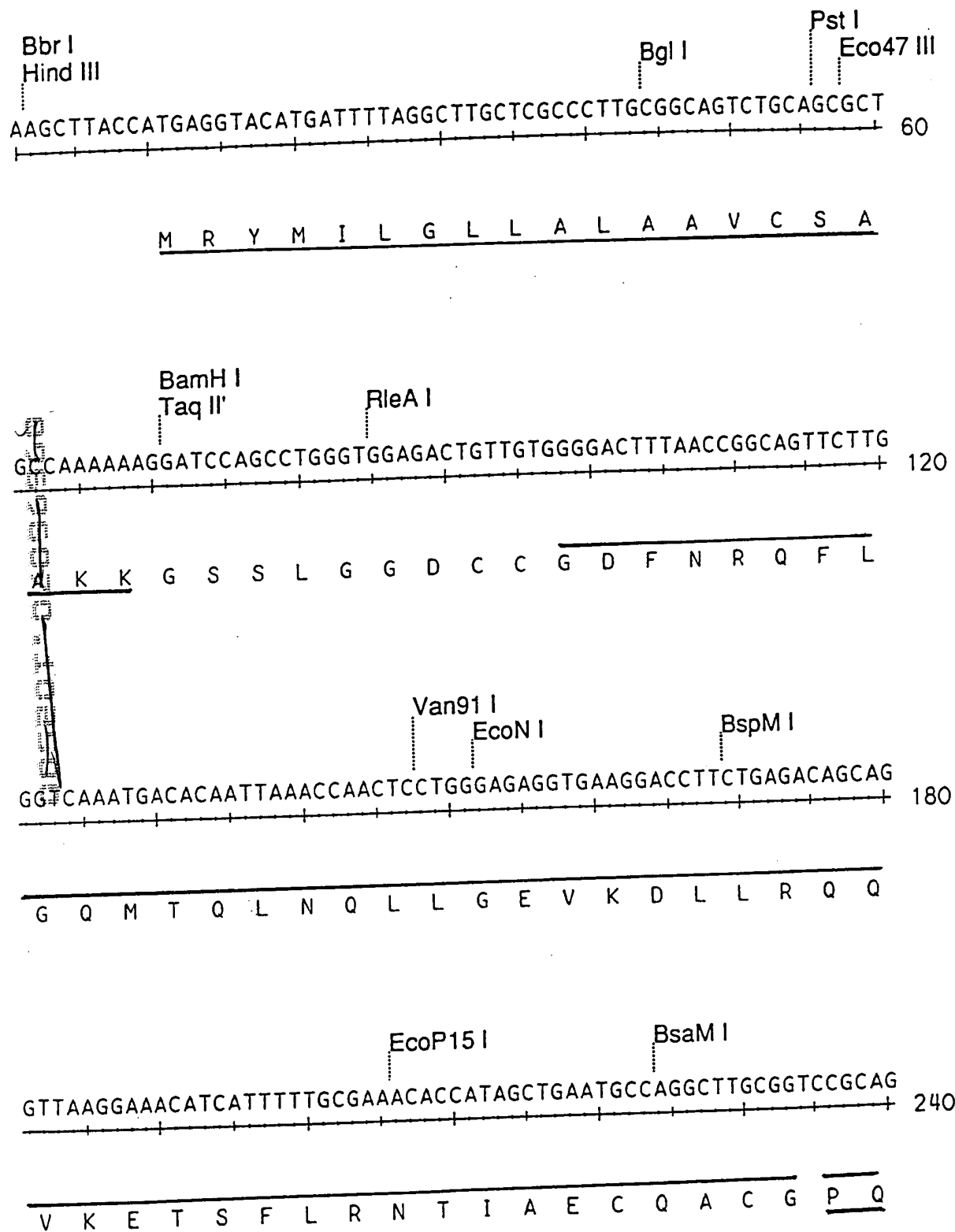


FIGURE 9C.

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CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

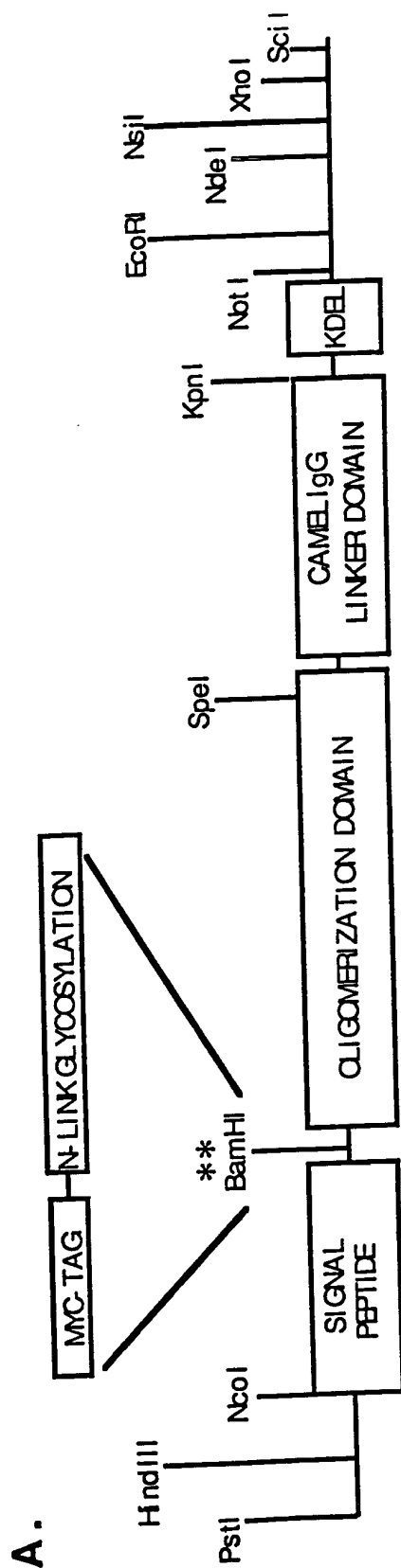
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360

P E G T G S S E K D E L .

Nsi I Xho I Scl I
CACTCGAG 369

FIGURE 9D.

Figure 10: KDEL Inhibitor Protein with myc-tag and a N-linked Glycosylation Sequence



B.

Signal cleavage site →

(myc-tag seq.)

N-link glycosylation seq.

MGKFTVVAALLLLGAVRAE-GS-EQKLISEEDL-YHPNSTC-GSS -

LGGDCC-PQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDACG-MQPARTPGTS-

PQPQKPQPQPQPQPKPEPE-GTGSSE-KDEL

Bbr I EcoP15 I
Hind III Nco I EcoP15 I
AAGCTTACCATGGGAAAGTTCACTGTGGTGGCGGCGGCGTTGCTGCTGCTGGGCGCGGTG 60

M G K F T V V A A A L L L L G A V

BamH I Bbs I Eco57 I
CGGGCCGAGGGATCCGAACAAAACTTATTTCTGAAGAAGACTTGTACCACCCAAACTCA 120

R A E G S E Q K L I S E E D L Y H P N S

Taq II' BamH I PshA I Bpm I
Taq II'
ACATGCGGATCCAGCCTGGGTGGAGACTGTTGTCCACAGATGCTTCGAGAACTCCAGGAG 180

T C G S S L G G D C C P Q M L R E L Q E

EcoICR I Sac I BspM I EclHK I BstZ2 I
ACTAATGCGGCGCTGCAAGACGTGAGAGAGCTCTTGCGACAGCAGGTCAAGGAGATCACC 240

T N A A L Q D V R E L L R Q Q V K E I T

FIGURE 10C.

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EcoP15 I Eco57 I BsaM I

TTCCTGAAGAATACGGTGATGGAATGTGACGCTTGCGGAATGCAGCCCGCACGCACCCCC 300

F L K N T V M E C D A C G M Q P A R T P

Spe I

GGTACTAGTCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCG 360

G T S P Q P Q P K P Q P Q P Q P Q P K P

Acc65 I Kpn I Eco52 I

CAGCCGAAACCGGAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG TAG GCGGCC 420

Q P K P E P E G T G S S E K D E L

EcoR I Nde I Ppu10 I BfrB I Nsi I Xho I Sci I

GCAGAATTCCATATGCATCTCGAG 444

FIGURE 10D.